

# BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

## X98077-SEQ ID NO:2 align

Results for:  ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

gi|1914699|emb|X98077.1|HBVCGWITY

**Description**

Hepatitis B virus complete genome, wild type

**Molecule type**

nucleic acid

**Query Length**

3215

**Subject ID**

1883

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

18

**Program**BLASTN 2.2.20+ [Citation](#)Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

## Search Parameters

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

## Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78



## Results Statistics

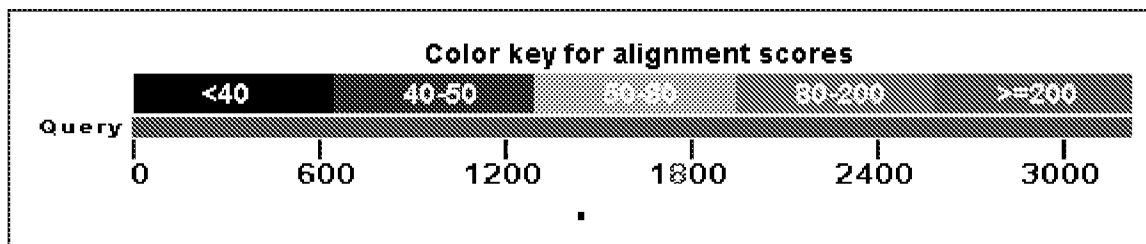
Effective search space 28854

### [Graphic Summary](#)

## Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Dot Matrix View](#)

# Plot of gi|1914699|emb|X98077.1|HBVCGWITY vs 1883

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



## Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

## Sequences producing significant alignments:

(Click headers to sort columns)

1883	33.7	33.7	0%	2e-06	100%
------	------	------	----	-------	------



[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>lcl|1883  
Length=18

Score = 33.7 bits (36), Expect = 2e-06  
Identities = 18/18 (100%), Gaps = 0/18 (0%)  
Strand=Plus/Plus

Query	1440	GCTGAATCCCGCGGACGA	1457
Sbjct	1	GCTGAATCCCGCGGACGA	18

[Select All](#) [Get selected sequences](#) [Distance tree of results](#)



# BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

## X98077-SEQ ID NO: 3

Results for:  ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

### Query ID

gi|1914699|emb|X98077.1|HBVCGWITY

### Description

Hepatitis B virus complete genome, wild type

### Molecule type

nucleic acid

### Query Length

3215

### Subject ID

3825

### Description

None

### Molecule type

nucleic acid

### Subject Length

21

### Program

BLASTN 2.2.20+ [Citation](#)

### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

## Search Parameters

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

## Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78



## Results Statistics

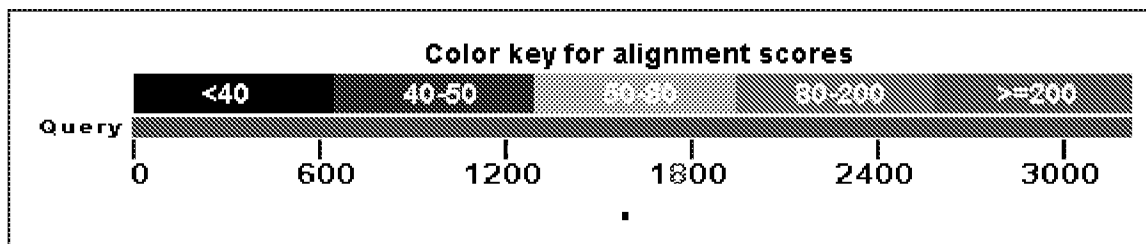
Effective search space 35255

### [Graphic Summary](#)

## Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Dot Matrix View](#)

## Plot of gi|1914699|emb|X98077.1|HBVCGWITY vs 3825 [\[?\]](#)

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



### [Descriptions](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

### Sequences producing significant alignments:

(Click headers to sort columns)

3825	33.7	33.7	0%	2e-06	95%
------	------	------	----	-------	-----



[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>lcl|3825  
Length=21

Score = 33.7 bits (36), Expect = 2e-06  
Identities = 20/21 (95%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query	1582	CACTTCGCTTCACCTCTGCAC	1602
Sbjct	1	CACTTCGCTTCACCTCAGCAC	21

[Select All](#) [Get selected sequences](#) [Distance tree of results](#)



# BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

## X98077-SEQ ID NO: 8

Results for:  ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

### Query ID

gi|1914699|emb|X98077.1|HBVCGWITY

### Description

Hepatitis B virus complete genome, wild type

### Molecule type

nucleic acid

### Query Length

3215

### Subject ID

63135

### Description

None

### Molecule type

nucleic acid

### Subject Length

22

### Program

BLASTN 2.2.20+ [Citation](#)

### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

## Search Parameters

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

## Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78



## Results Statistics

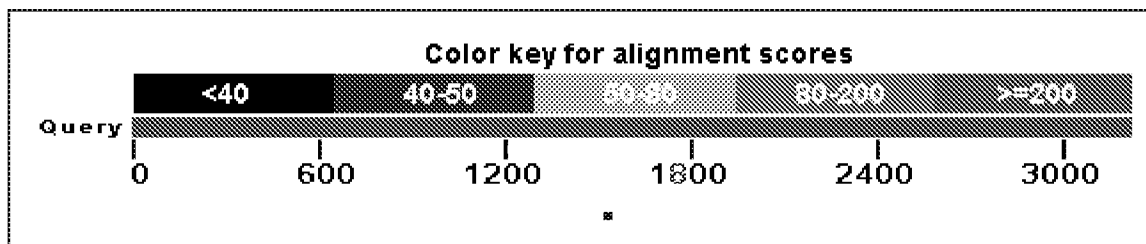
Effective search space 38460

### [Graphic Summary](#)

## Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Dot Matrix View](#)

## Plot of gi|1914699|emb|X98077.1|HBVCGWITY vs 63135 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



### Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

### Sequences producing significant alignments:

(Click headers to sort columns)

63135	41.0	41.0	0%	2e-08	100%
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[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>lcl|63135  
Length=22

Score = 41.0 bits (44), Expect = 2e-08  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Plus

Query	1527	CACCTCTCTTTACGCGGACTCC	1548
Sbjct	1	CACCTCTCTTTACGCGGACTCC	22

[Select All](#) [Get selected sequences](#) [Distance tree of results](#)